

SCORE Search Results Details for Application 10828332 and Search Result us-10-828-332-6.rnpm.

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OM nucleic - nucleic search, using sw model

Run on: April 26, 2006, 03:25:21 ; Search time 10101 Seconds
(without alignments)
9606.645 Million cell updates/sec

Title: US-10-828-332-6

Perfect score: 1755

Sequence: 1 atgccagggtatcatcatc.....acaccaaccatgccatctag 1755

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 158295336

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

1: /cgn2_6/ptodata/1/pna/PCTUSA_COMB.seq:*

2: /cgn2_6/ptodata/1/pna/PCTUSB_COMB.seq:*

3: /cgn2_6/ptodata/1/pna/PCTUSC_COMB.seq:*

4: /cgn2_6/ptodata/1/pna/US06_COMB.seq:*

5: /cgn2_6/ptodata/1/pna/US075_COMB.seq:*

6: /cgn2_6/ptodata/1/pna/US076_COMB.seq:*

7: /cgn2_6/ptodata/1/pna/US077_COMB.seq:*

8: /cgn2_6/ptodata/1/pna/US078_COMB.seq:*

9: /cgn2_6/ptodata/1/pna/US079_COMB.seq:*

10: /cgn2_6/ptodata/1/pna/US080_COMB.seq:*

11: /cgn2_6/ptodata/1/pna/US081_COMB.seq:*

12: /cgn2_6/ptodata/1/pna/US082_COMB.seq:*

13: /cgn2_6/ptodata/1/pna/US083_COMB.seq:*

14: /cgn2_6/ptodata/1/pna/US084_COMB.seq:*

15: /cgn2_6/ptodata/1/pna/US085_COMB.seq:*

16: /cgn2_6/ptodata/1/pna/US086_COMB.seq:*

SCORE Search Results Details for Application 10828332 and Search Result us-10-828-332- 6.rnnpn.

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OM nucleic - nucleic search, using sw model

Run on: April 26, 2006, 03:27:02 ; Search time 722 Seconds
(without alignments)
7897.181 Million cell updates/sec

Title: US-10-828-332-6

Perfect score: 1755

Sequence: 1 atgccagggttatcatcatc.....acaccaaccatgccatctag 1755

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7549803 seqs, 1624434298 residues

Total number of hits satisfying chosen parameters: 15099606

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:
1: /SIDS5/ptodata/1/pna/PCT_NEW_COMB.seq:*

2: /SIDS5/ptodata/1/pna/US06_NEW_COMB.seq:*

3: /SIDS5/ptodata/1/pna/US07_NEW_COMB.seq:*

4: /SIDS5/ptodata/1/pna/US08_NEW_COMB.seq:*

5: /SIDS5/ptodata/1/pna/US09_NEW_COMB.seq:*

6: /SIDS5/ptodata/1/pna/US10_NEW_COMB.seq:*

7: /SIDS5/ptodata/1/pna/US10_NEW_COMB.seq1:*

8: /SIDS5/ptodata/1/pna/US11_NEW_COMB.seq:*

9: /SIDS5/ptodata/1/pna/US11_NEW_COMB.seq1:*

10: /SIDS5/ptodata/1/pna/US11_NEW_COMB.seq2:*

11: /SIDS5/ptodata/1/pna/US11_NEW_COMB.seq3:*

12: /SIDS5/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	3	gabriel near ana	US-PGPUB; USPAT; DERWENT	OR	ON	2006/10/02 09:04
L2	1	gabriel near san near ana	US-PGPUB; USPAT; DERWENT	OR	ON	2006/10/02 08:44
L3	1809	gabriel near san	US-PGPUB; USPAT; DERWENT	OR	ON	2006/10/02 08:44
L4	6	maekawa near takami	US-PGPUB; USPAT; DERWENT	OR	ON	2006/10/02 09:04
L5	14	uneyama near hisayuki	US-PGPUB; USPAT; DERWENT	OR	ON	2006/10/02 09:05
L6	17	l1 or l2 or l4 or l5	US-PGPUB; USPAT; DERWENT	OR	ON	2006/10/02 09:05
L7	6	l6 and glutamic	US-PGPUB; USPAT; DERWENT	OR	ON	2006/10/02 09:08
L8	5029	glutamic adj acid.clm.	US-PGPUB; USPAT; DERWENT	OR	ON	2006/10/02 09:08
L9	390	l8 and receptor.clm.	US-PGPUB; USPAT; DERWENT	OR	ON	2006/10/02 09:10
L10	14	l9 and metabotrop\$3	US-PGPUB; USPAT; DERWENT	OR	ON	2006/10/02 09:10

=> d his

(FILE 'HOME' ENTERED AT 09:13:08 ON 02 OCT 2006)

FILE 'MEDLINE, CAPLUS, BIOSIS' ENTERED AT 09:13:26 ON 02 OCT 2006

L1 20033 S METABOTROP?

L2 18304 S L1 (P) GLUTAM?

L3 18203 S L2 (P) RECEPTOR

L4 0 S L3 AND GABRIEL

L5 17057 S L3 AND GLUTAMATE (1W) RECEPTOR

L6 17003 S L5 AND METABOTROPIC

L7 9227 DUP REM L6 (7776 DUPLICATES REMOVED)

L8 0 S L7 AND PU<2000

L9 4049 S L7 AND PY<2000

L10 2654 S L9 AND PY>1995

L11 743 S L10 AND PY>1998

L12 0 S L11 AND SEQ NEAR ID

L13 67 S L11 AND SEQUENCE

L14 10 S L13 AND MRNA
E GABRIEL ANA S /AU
E GABRIEL SAN /AU
E MAEKAWA TAKAMI /AU
E UNEYAMA HISAYUKI /AU

L15 14284 S E 3
E MAEKAWA TAKAMI /AU

L16 17 S E3

L17 1 S L16 AND GLUTAMIC

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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 25, 2006, 12:46:23 ; Search time 160.3 Seconds
(without alignments)
3025.990 Million cell updates/sec

Title: US-10-828-332-6
Perfect score: 3303
Sequence: 1 atgccagggtatcatcatc.....acaccaaccatgccatctag 1755

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7861189 seqs, 1381955077 residues

Total number of hits satisfying chosen parameters: 15722378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

```
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10828332/runat_25042006_092247_27363/app_query.fasta_1
-DB=Pending_Patents_AA_Main -QFMT=fastan -SUFFIX=rapm -MINMATCH=0.1 -LOOPCL=0
-LOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss02p -USER=US10828332@CGN_1_1_1104@runat_25042006_092247_27363
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : Pending_Patents_AA_Main:*

```
1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US066_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US073_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US074_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US075_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US076_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US077_COMB.pep:*
8: /cgn2_6/ptodata/1/paa/US078_COMB.pep:*
9: /cgn2_6/ptodata/1/paa/US079_COMB.pep:*
10: /cgn2_6/ptodata/1/paa/US080_COMB.pep:*
11: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
12: /cgn2_6/ptodata/1/paa/US082_COMB.pep:*
```

```

13: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*
14: /cgn2_6/ptodata/1/paa/US084_COMB.pep:*
15: /cgn2_6/ptodata/1/paa/US085_COMB.pep:*
16: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*
17: /cgn2_6/ptodata/1/paa/US087_COMB.pep:*
18: /cgn2_6/ptodata/1/paa/US088_COMB.pep:*
19: /cgn2_6/ptodata/1/paa/US089_COMB.pep:*
20: /cgn2_6/ptodata/1/paa/US090_COMB.pep:*
21: /cgn2_6/ptodata/1/paa/US091_COMB.pep:*
22: /cgn2_6/ptodata/1/paa/US092_COMB.pep:*
23: /cgn2_6/ptodata/1/paa/US093_COMB.pep:*
24: /cgn2_6/ptodata/1/paa/US094_COMB.pep:*
25: /cgn2_6/ptodata/1/paa/US095_COMB.pep:*
26: /cgn2_6/ptodata/1/paa/US096_COMB.pep:*
27: /cgn2_6/ptodata/1/paa/US097_COMB.pep:*
28: /cgn2_6/ptodata/1/paa/US098_COMB.pep:*
29: /cgn2_6/ptodata/1/paa/US099_COMB.pep:*
30: /cgn2_6/ptodata/1/paa/US100_COMB.pep:*
31: /cgn2_6/ptodata/1/paa/US101_COMB.pep:*
32: /cgn2_6/ptodata/1/paa/US102_COMB.pep:*
33: /cgn2_6/ptodata/1/paa/US103_COMB.pep:*
34: /cgn2_6/ptodata/1/paa/US104_COMB.pep:*
35: /cgn2_6/ptodata/1/paa/US105_COMB.pep:*
36: /cgn2_6/ptodata/1/paa/US106_COMB.pep:*
37: /cgn2_6/ptodata/1/paa/US107_COMB.pep:*
38: /cgn2_6/ptodata/1/paa/US108_COMB.pep:*
39: /cgn2_6/ptodata/1/paa/US109_COMB.pep:*
40: /cgn2_6/ptodata/1/paa/US110_COMB.pep:*
41: /cgn2_6/ptodata/1/paa/US111_COMB.pep:*
42: /cgn2_6/ptodata/1/paa/US112_COMB.pep:*
43: /cgn2_6/ptodata/1/paa/US114_COMB.pep:*
44: /cgn2_6/ptodata/1/paa/US600_COMB.pep:*
45: /cgn2_6/ptodata/1/paa/US601_COMB.pep:*
46: /cgn2_6/ptodata/1/paa/US602_COMB.pep:*
47: /cgn2_6/ptodata/1/paa/US603_COMB.pep:*
48: /cgn2_6/ptodata/1/paa/US604_COMB.pep:*
49: /cgn2_6/ptodata/1/paa/US605_COMB.pep:*
50: /cgn2_6/ptodata/1/paa/US606_COMB.pep:*
51: /cgn2_6/ptodata/1/paa/US607_COMB.pep:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	3107	94.1	584	38	US-10-828-332-7	Sequence 7, Appli
2	3050.5	92.4	912	32	US-10-219-051B-4035	Sequence 4035, Ap
3	3050.5	92.4	912	32	US-10-219-051B-4039	Sequence 4039, Ap
4	3004.5	91.0	704	39	US-10-932-333-1999	Sequence 1999, Ap
5	3004.5	91.0	704	49	US-60-500-315-1999	Sequence 1999, Ap
6	3004.5	91.0	909	26	US-09-679-664-48	Sequence 48, Appli
7	3004.5	91.0	912	1	PCT-US04-00750-66	Sequence 66, Appli
8	3004.5	91.0	912	18	US-08-816-178A-2	Sequence 2, Appli

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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 25, 2006, 12:46:47 ; Search time 20.5 Seconds
(without alignments)
2553.097 Million cell updates/sec

Title: US-10-828-332-6
Perfect score: 3303
Sequence: 1 atgccagggtatcatcatc.....acaccaaccatgccatctag 1755

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 629085 seqs, 149112515 residues

Total number of hits satisfying chosen parameters: 1258170

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

```
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10828332/runat_25042006_092249_27375/app_query.fasta_1
-DB=Pending_Patents_AA_New -QFMT=fastan -SUFFIX=rapn -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss02p -USER=US10828332@CGN_1_1_107@runat_25042006_092249_27375
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : Pending_Patents_AA_New:*

- 1: /SIDSS5/ptodata/1/paa/PCT_NEW_COMB.pep:*
- 2: /SIDSS5/ptodata/1/paa/US06_NEW_COMB.pep:*
- 3: /SIDSS5/ptodata/1/paa/US07_NEW_COMB.pep:*
- 4: /SIDSS5/ptodata/1/paa/US08_NEW_COMB.pep:*
- 5: /SIDSS5/ptodata/1/paa/US09_NEW_COMB.pep:*
- 6: /SIDSS5/ptodata/1/paa/US10_NEW_COMB.pep:*
- 7: /SIDSS5/ptodata/1/paa/US11_NEW_COMB.pep:*
- 8: /SIDSS5/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
1	2219	67.2	915	8	US-60-732-162-1552	Sequence 1552, Ap
2	2210	66.9	915	6	US-11-344-728-2	Sequence 2, Appli
3	2191.5	66.3	922	8	US-60-732-162-1554	Sequence 1554, Ap
4	2189	66.3	913	8	US-60-732-162-1556	Sequence 1556, Ap
5	2054	62.2	877	6	US-11-214-063A-1132	Sequence 1132, Ap
6	1284.5	38.9	1520	6	US-11-214-063A-630	Sequence 630, App
7	1283	38.8	364	6	US-11-293-697-4612	Sequence 4612, Ap
8	1131	34.2	1194	6	US-10-567-867-636	Sequence 636, App
9	1131	34.2	1194	8	US-60-751-420-1596	Sequence 1596, Ap
10	1123	34.0	1180	1	PCT-US06-13172-7	Sequence 7, Appli
11	1123	34.0	1180	8	US-60-742-219-2500	Sequence 2500, Ap
12	1121.5	34.0	878	7	US-11-404-939-347	Sequence 347, App
13	1113	33.7	1199	6	US-11-271-139-2	Sequence 2, Appli
C	14	873	26.4	297	6	US-10-498-451-1262
	15	528	16.0	297	7	US-11-360-355-120729
	16	521	15.8	684	7	US-11-360-355-120999
	17	428.5	13.0	839	8	US-60-751-420-42
	18	427.5	12.9	879	6	US-11-214-063A-454
	19	426.5	12.9	929	6	US-11-214-063A-868
	20	359.5	10.9	936	6	US-11-214-063A-602
	21	313.5	9.5	371	7	US-11-360-355-120501
	22	299	9.1	4315	6	US-10-461-673-9612
	23	282.5	8.6	595	8	US-60-742-219-2100
	24	282.5	8.6	755	6	US-11-214-063A-450
	25	277.5	8.4	413	7	US-11-056-355B-4735
	26	271	8.2	7285	6	US-11-272-521-28
	27	265	8.0	493	7	US-11-056-355B-65494
	28	262	7.9	375	7	US-11-056-355B-3621
	29	261.5	7.9	519	7	US-11-056-355B-6752
	30	259.5	7.9	487	7	US-11-056-355B-6753
	31	258.5	7.8	3682	7	US-11-174-307B-2486
	32	251.5	7.6	2757	7	US-11-174-307B-1642
	33	249.5	7.6	502	6	US-10-461-673-12610
	34	247	7.5	4440	6	US-10-184-614A-525
	35	247	7.5	4440	6	US-10-184-615A-525
	36	245.5	7.4	1659	7	US-11-174-307B-3184
	37	243	7.4	2118	6	US-11-192-046-125
	38	243	7.4	2578	6	US-10-244-081A-31
	39	242.5	7.3	1269	7	US-11-174-307B-164
	40	242.5	7.3	1356	7	US-11-174-307B-64
	41	242	7.3	291	7	US-11-056-355B-3800
	42	241.5	7.3	3259	7	US-11-174-307B-1020
	43	241.5	7.3	3259	7	US-11-174-307B-2622
	44	241.5	7.3	4243	7	US-11-174-307B-1722
	45	241	7.3	473	1	PCT-US06-07136-166

ALIGNMENTS

RESULT 1
US-60-732-162-1552